

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/532,441

Source: PT 10

Date Processed by STIC: 5/3/05

ENTERED

DATE: 05/03/2005

TIME: 11:48:30

Output Set: N:\CRF4\05032005\J532441.raw

6 Thereof as a Treatment for Infectious Diseases

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/532,441

10 <150> PRIOR APPLICATION NUMBER: PCT/US03/33524

11 <151> PRIOR FILING DATE: 2003-10-22

13 <150> PRIOR APPLICATION NUMBER: US 60/420,131

14 <151> PRIOR FILING DATE: 2002-10-22

16 <160> NUMBER OF SEQ ID NOS: 12

18 <170> SOFTWARE: PatentIn version 3.2

20 <210> SEQ ID NO: 1

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21 <211> LENGTH: 463
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22 <212> TYPE: PRT

23 <213> ORGANISM: M. tuberculosis H37Rv

25 <400> SEQUENCE: 1

27 Met Ser Pro Gln Gln Glu Pro Thr Ala Gln Pro Pro Arg Arg His Arg

28 1 5 10 15

31 Val Val Ile Ile Gly Ser Gly Phe Gly Gly Leu Asn Ala Ala Lys Lys

32 20 25 30

35 Leu Lys Arg Ala Asp Val Asp Ile Lys Leu Ile Ala Arg Thr Thr His

36 35 40 45

39 His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Ile Ser

40 50 55 60

43 Glu Gly Glu Ile Ala Pro Pro Thr Arg Val Val Leu Arg Lys Gln Arg

44 65 70 75 80

47 Asn Val Gln Val Leu Leu Gly Asn Val Thr His Ile Asp Leu Ala Gly

48 85 90 95

51 Gln Cys Val Val Ser Glu Leu Leu Gly His Thr Tyr Gln Thr Pro Tyr

52 100 105 110

55 Asp Ser Leu Ile Val Ala Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn

56 115 120 125

59 Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala

[illegible]

63 Leu Glu Leu Arg Gly Arg Ile Leu Ser Ala Phe Glu Gln Ala Glu Arg

64 145 150 155 160

67 Ser Ser Asp Pro Glu Arg Arg Ala Lys Leu Leu Thr Phe Thr Val Val

68 165 170 175

71 Gly Ala Gly Pro Thr Gly Val Glu Met Ala Gly Gln Ile Ala Glu Leu

72 180 185 190

75 Ala Glu His Thr Leu Lys Gly Ala Phe Arg His Ile Asp Ser Thr Lys

76 195 200 205

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80      210                      215                      220
83 Gly Ala Lys Leu Gly Gln Arg Ala Ala Ala Arg Leu Gln Lys Leu Gly
84 225                      230                      235                      240
87 Val Glu Ile Gln Leu Gly Ala Met Val Thr Asp Val Asp Arg Asn Gly
88      245                      250                      255
91 Ile Thr Val Lys Asp Ser Asp Gly Thr Val Arg Arg Ile Glu Ser Ala
92      260                      265                      270
95 Cys Lys Val Trp Ser Ala Gly Val Ser Ala Ser Arg Leu Gly Arg Asp
96      275                      280                      285
99 Leu Ala Glu Gln Ser Arg Val Glu Leu Asp Arg Ala Gly Arg Val Gln
100     290                      295                      300
103 Val Leu Pro Asp Leu Ser Ile Pro Gly Tyr Pro Asn Val Phe Val Val
104 305                      310                      315                      320
107 Gly Asp Met Ala Ala Val Glu Gly Val Pro Gly Val Ala Gln Gly Ala
108      325                      330                      335
111 Ile Gln Gly Ala Lys Tyr Val Ala Ser Thr Ile Lys Ala Glu Leu Ala
112      340                      345                      350
115 Gly Ala Asn Pro Ala Glu Arg Glu Pro Phe Gln Tyr Phe Asp Lys Gly
116      355                      360                      365
119 Ser Met Ala Thr Val Ser Arg Phe Ser Ala Val Ala Lys Ile Gly Pro
120      370                      375                      380
123 Val Glu Phe Ser Gly Phe Ile Ala Trp Leu Ile Trp Leu Val Leu His
124 385                      390                      395                      400
127 Leu Ala Tyr Leu Ile Gly Phe Lys Thr Lys Ile Thr Thr Leu Leu Ser
128      405                      410                      415
131 Trp Thr Val Thr Phe Leu Ser Thr Arg Arg Gly Gln Leu Thr Ile Thr
132      420                      425                      430
135 Asp Gln Gln Ala Phe Ala Arg Thr Arg Leu Glu Gln Leu Ala Glu Leu
136      435                      440                      445
139 Ala Ala Glu Ala Gln Gly Ser Ala Ala Ser Ala Lys Val Ala Ser
140      450                      455                      460
143 <210> SEQ ID NO: 2
144 <211> LENGTH: 1392
145 <212> TYPE: DNA
146 <213> ORGANISM: M. tuberculosis H37Rv
148 <400> SEQUENCE: 2
149 atgagtcccc agcaagaacc cacagcgcaa ccacctcgta ggcacgcagt tgtgatcatc      60
151 ggatctgggt tcggcgggct aaacgcggca aagaagctca agcgggcca cgttgacatc      120
153 aagctgatcg cgcgcaccac ccacacctg ttccagccgc tgctgtacca agtggccacc      180
155 gggattatct ccgagggaga aatcgctccg ccgacccggg tcgtgctgcg taagcagcgc      240
157 aatgtccagg tactgttggg caacgtcacc cacatcgacc tggccgggca gtgcgtcgtc      300
159 tcggaattgc tcggtcacac ctaccaaacc ccctacgaca gcctgatcgt cgccgcgggt      360
161 gctggccagt cttatttcgg caacgaccat ttgcgcgaat tcgcacccgg catgaagtcc      420
163 atcgacgacg cgttgagggt gcgtggccgc atattgagcg ctttcgagca agccgaacgg      480
165 tccagcgatc cggaacggcg ggccaagcta ctgacattca ccgttgctcg ggctggcccc      540
167 accggtgttg aaatggccgg acagatcgcc gagctggccg agcacacggt gaagggcgca      600
169 ttccggcaca tcgactcgac caaggcgcgg gtgattctgc ttgacgccgc cccggcggtg      660
171 ctgccaccga tgggcgcaaa gctcggtcag cgggcggctg cccggttgca gaagctgggc      720

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173 gtggaaatcc agctgggtgc gatggtcacc gacgtcgacc gcaacggcat caccgtcaag      780
175 gactccgacg gcaccgtccg gcgcacgcag tcggcctgca aggtctggtc ggccgggggtt      840
177 tcggccagtc ggttgggcag ggaccttgcc gagcaatcac gggttgagct cgaccggggcc      900
179 ggccgggtcc aagtgtgtcc cgacctgtcc attcccgggt acccgaacgt gttcgtgggtg      960
181 ggcgatatgg ccgctgtgga ggggtgtgcc ggtgtggcgc agggcgccat ccagggggcg      1020
183 aaatacgtcg ccagcacgat caaggccgaa ctggccggcg ccaaccggc ggagcgtgag      1080
185 ccattccagt acttcgacaa gggatcgatg gccacggttt cgaggttttc ggcggtggcc      1140
187 aagatcggtc ccgttgagtt cagcggtttt atcgcttggc tgatttggct ggtgctgcac      1200
189 ctggcgtacc tgatcgggtt caagaccaag atcaccactc tgctgtcgtg gacggtgact      1260
191 ttcctcagta ctgcgcgcgg ccagctgacc atcaccgacc agcaggcatt tgcgcgaacg      1320
193 cggctcgaac agctggccga gctggccgcc gaggcgcagg gctcagcggc aagcgctaag      1380
195 gtggccagct ag                                         1392
198 <210> SEQ ID NO: 3
199 <211> LENGTH: 470
200 <212> TYPE: PRT
201 <213> ORGANISM: M. tuberculosis H37Rv
203 <400> SEQUENCE: 3
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206 1 5 10 15
209 Val Val Ile Ile Gly Ser Gly Phe Gly Gly Leu Asn Ala Ala Lys Ala
210 20 25 30
213 Leu Lys Arg Ala Asp Val Asp Ile Thr Leu Ile Ser Lys Thr Thr Thr
214 35 40 45
217 His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser
218 50 55 60
221 Glu Gly Asp Ile Ala Pro Thr Thr Arg Leu Ile Leu Arg Arg Gln Lys
222 65 70 75 80
225 Asn Val Arg Val Leu Leu Gly Glu Val Asn Ala Ile Asp Leu Lys Ala
226 85 90 95
229 Gln Thr Val Thr Ser Lys Leu Met Asp Met Thr Thr Val Thr Pro Tyr
230 100 105 110
233 Asp Ser Leu Ile Val Ala Ala Gly Ala Gln Gln Ser Tyr Phe Gly Asn
234 115 120 125
237 Asp Glu Phe Ala Thr Phe Ala Pro Gly Met Lys Thr Ile Asp Asp Ala
238 130 135 140
241 Leu Glu Leu Arg Gly Arg Ile Leu Gly Ala Phe Glu Ala Ala Glu Val
242 145 150 155 160
245 Ser Thr Asp His Ala Glu Arg Glu Arg Arg Leu Thr Phe Val Val Val
246 165 170 175
249 Gly Ala Gly Pro Thr Gly Val Glu Val Ala Gly Gln Ile Val Glu Leu
250 180 185 190
253 Ala Glu Arg Thr Leu Ala Gly Ala Phe Arg Thr Ile Thr Pro Ser Glu
254 195 200 205
257 Cys Arg Val Ile Leu Leu Asp Ala Ala Pro Ala Val Leu Pro Pro Met
258 210 215 220
261 Gly Pro Lys Leu Gly Leu Lys Ala Gln Arg Arg Leu Glu Lys Met Asp
262 225 230 235 240
265 Val Glu Val Gln Leu Asn Ala Met Val Thr Ala Val Asp Tyr Lys Gly
266 245 250 255

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269 Ile Thr Ile Lys Glu Lys Asp Gly Gly Glu Arg Arg Ile Glu Cys Ala
270           260           265           270
273 Cys Lys Val Trp Ala Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Met
274           275           280           285
277 Ile Ala Glu Gly Ser Asp Gly Thr Glu Ile Asp Arg Ala Gly Arg Val
278           290           295           300
281 Ile Val Glu Pro Asp Leu Thr Val Lys Gly His Pro Asn Val Phe Val
282 305           310           315           320
285 Val Gly Asp Leu Met Phe Val Pro Gly Val Pro Gly Val Ala Gln Gly
286           325           330           335
289 Ala Ile Gln Gly Ala Arg Tyr Ala Thr Thr Val Ile Lys His Met Val
290           340           345           350
293 Lys Gly Asn Asp Asp Pro Ala Asn Arg Lys Pro Phe His Tyr Phe Asn
294           355           360           365
297 Lys Gly Ser Met Ala Thr Ile Ser Arg His Ser Ala Val Ala Gln Val
298           370           375           380
301 Gly Lys Leu Glu Phe Ala Gly Tyr Phe Ala Trp Leu Ala Trp Leu Val
302 385           390           395           400
305 Leu His Leu Val Tyr Leu Val Gly Tyr Arg Asn Arg Ile Ala Ala Leu
306           405           410           415
309 Phe Ala Trp Gly Ile Ser Phe Met Gly Arg Ala Arg Gly Gln Met Ala
310           420           425           430
313 Ile Thr Ser Gln Met Ile Tyr Ala Arg Leu Val Met Thr Leu Met Glu
314           435           440           445
317 Gln Gln Ala Gln Gly Ala Leu Ala Ala Ala Glu Gln Ala Glu His Ala
318           450           455           460
321 Glu Gln Glu Ala Ala Gly
322 465           470

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325 <210> SEQ ID NO: 4

326 <211> LENGTH: 1413

327 <212> TYPE: DNA

328 <213> ORGANISM: M. tuberculosis H37Rv

330 <400> SEQUENCE: 4

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331 atgacgctct catctggtga accctcggcc gtcggcgggc gccatcgcgt ggtcatcatc      60
333 ggtagtggat tcggcggcct gaatgcggcc aaggcgctta aacgggcgga tgcgacatc      120
335 acgctgatct ccaagacaac gaccacctg ttccagccgc tgctgtatca agtggccacc      180
337 gggatcttgt ccgagggcga cattgccccg accacccggc tgatcctgcg ccggcaaaaag      240
339 aacgtccggg tgttgctggg cgagggtcaac gcgatcgacc tgaaaagcgca gacggtcacg      300
341 tcgaaattga tggacatgac cacggtgacg ccgtacgaca gcctcatcgt ggccgccggc      360
343 gcacagcagt cctacttcgg caacgacgaa ttcgccacct tcgcgcccgg aatgaagacc      420
345 atcgacgacg cgctggagct gcgcggccgc atcctgggcg cgttcgaggc cgccgaggtc      480
347 agcaccgacc atgccgaacg ggagcggcgc ctgacgttcg tcgtcgtcgg cgctgggccc      540
349 accggcgctc aggtggctgg gcagatcgtc gagctcgccg agcgcaccct ggcaggcgcg      600
351 tttaggacca tcacgccag tgagtgcggg gtgacctcgc tcgacgccgc acccgcggtg      660
353 ttgccgccga tgggtccaaa gctgggtctc aaggcacaac ggcggctgga aaagatggac      720
355 gtcgaggttc aactcaacgc gatggtgacc gcggtcgact acaaaggcat caccatcaag      780
357 gaaaaggacg gcggcgaacg ccgcatcgaa tgcgcgtgca aggtttgggc ggccggcgctg      840
359 gcggccaagg cgctgggcaa gatgatcgcc gagggatccg acggaaccga aatcgaccgg      900
361 gccggaaggg tgatcgtgga acccgatctc accgtcaagg gacatccgaa cgtcttcgta      960

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363 gtcggcgatc tgatgttcgt gcccggcgta cccgggggtgg ctccaggcgc gatccagggg 1020
365 gcccgatacg ccaccacggt gatcaaacac atgggtcaagg gcaatgacga cccagccaat 1080
367 cgcaagccgt tccattactt caacaagggc agcatggcga cgatctcccg ccacagcgcc 1140
369 gtcgcgcagg tcggcaagct ggagtttgcc ggggtacttcg cctgggtggc gtggctggtg 1200
371 ctgcacctgg tctacctggt cggtatcgg aaccgcacgc cagccctggt cgctggggg 1260
373 atctccttca tgggcccgcgc ccgcggccag atggccatca ccagccagat gatctacgcc 1320
375 aggttagtga tgaccttgat ggaacagcag gcacaaggag cgctggcagc cgccgaacag 1380
377 gccgagcacg ccgagcaaga ggcagcgggt tag 1413

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380 <210> SEQ ID NO: 5

381 <211> LENGTH: 219

382 <212> TYPE: PRT

383 <213> ORGANISM: M. tuberculosis CDC1551

385 <400> SEQUENCE: 5

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387 Met Phe Asp Gly Val Ala Arg Lys Tyr Asp Leu Thr Asn Thr Val Leu
388 1 5 10 15
391 Ser Leu Gly Gln Asp Arg Tyr Trp Arg Arg Ala Thr Arg Ser Ala Leu
392 20 25 30
395 Arg Ile Gly Pro Gly Gln Lys Val Leu Asp Leu Ala Ala Gly Thr Ala
396 35 40 45
399 Val Ser Thr Val Glu Leu Thr Lys Ser Gly Ala Trp Cys Val Ala Ala
400 50 55 60
403 Asp Phe Ser Val Gly Met Leu Ala Ala Gly Ala Ala Arg Lys Val Pro
404 65 70 75 80
407 Lys Val Ala Gly Asp Ala Thr Arg Leu Pro Phe Gly Asp Asp Val Phe
408 85 90 95
411 Asp Ala Val Thr Ile Ser Phe Gly Leu Arg Asn Val Ala Asn Gln Gln
412 100 105 110
415 Ala Ala Leu Arg Glu Met Ala Arg Val Thr Arg Pro Gly Gly Arg Leu
416 115 120 125
419 Leu Val Cys Glu Phe Ser Thr Pro Thr Asn Ala Leu Phe Ala Thr Ala
420 130 135 140
423 Tyr Lys Glu Tyr Leu Met Arg Ala Leu Pro Arg Val Ala Arg Ala Val
424 145 150 155 160
427 Ser Ser Asn Pro Glu Ala Tyr Glu Tyr Leu Ala Glu Ser Ile Arg Ala
428 165 170 175
431 Trp Pro Asp Gln Ala Val Leu Ala His Gln Ile Ser Arg Ala Gly Trp
432 180 185 190
435 Ser Gly Val Arg Trp Arg Asn Leu Thr Gly Gly Ile Val Ala Leu His
436 195 200 205
439 Ala Gly Tyr Lys Pro Gly Lys Gln Thr Pro Gln
440 210 215

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443 <210> SEQ ID NO: 6

444 <211> LENGTH: 660

445 <212> TYPE: DNA

446 <213> ORGANISM: M. tuberculosis CDC1551

448 <400> SEQUENCE: 6

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449 atgttcgatg gcgtcgcccc caagtatgac ctgaccaata ccgtgttgtc cctggggccag 60
451 gaccgggtatt ggcgggcgagc cactcggtcg gcgctgcgga tcgggccccg caaaagggtc 120
453 ctggacctgg ccgcgggcac cgccgtgtcc accgtagagc tcaccaaata gggcgcggtg 180

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/532,441

DATE: 05/03/2005

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date